



SEQUENCE LISTING

#8

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Nolan, Garry P.
Rothenberg, Michael S.
- (ii) TITLE OF INVENTION: Methods for Screening for Transdominant
Effector Peptides and RNA Molecules
- 10 (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
(B) STREET: 4 Embarcadero Center, Suite 3400
(C) CITY: San Francisco
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111-4187
- 20 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/589,109
(B) FILING DATE: 23-JAN-1996
30 (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Silva, Robin M.
(B) REGISTRATION NUMBER: 38,304
35 (C) REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (415) 781-1989
(B) TELEFAX: (415) 949-8711
40

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
50
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa
1 5

55

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTTAGCAAG ATCTCTACGG TGGACCKNNK NNNNNNNNNK NNNNNNNNNK KNNNNNNCCCC 60

15 ACTCCCATGG TCCTACGTAC CACCACACTG GG 92

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTTAGCAAG ATCTGTGTGT CAGTTAGGGT GTGG 34

30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGAGAACC AGGACCATGG GCNNNNNNNN KNNNNNNNNK NNNNNNNNNK NKGGGGCCCCC 60

45 TTAAACCATT AAAT 74

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGGAGAACC AGGACCATGG GCNNKNNKNN KCCTCCCNK CCTNNKNNKG GGCCCCCTTA 60
5 AACCATTAAA T 71

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCATGCATCC AATTTAATGG TTTAAG 26
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 4950 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCAT 60
35 GGAAATACA TAACTGAGAA TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCA 120
GAATATGGGC CAAACAGGAT ATCTGTGGTA AGCAGTTCCT GCCCCGGCTC AGGGCCAAGA 180
ACAGATGGTC CCCAGATGCG GTCCCGCCCT CAGCAGTTTC TAGAGAACCA TCAGATGTTT 240
40 CCAGGGTGCC CCAAGGACCT GAAAATGACC CTGTGCCTTA TTTGAACTAA CCAATCAGTT 300
CGCTTCTCGC TTCTGTTCGC GCGCTTCTGC TCCCGAGCT CAATAAAGA GCCCACAACC 360
45 CCTCACTCGG CGCGCCAGTC CTCCGATAGA CTGCGTCGCC CGGGTACCCG TATTCCCAAT 420
AAAGCCTCTT GCTGTTTGCA TCCGAATCGT GGACTCGCTG ATCCTTGGGA GGGTCTCCTC 480
AGATTGATTG ACTGCCCACC TCGGGGGTCT TTCATTGGA GGTTCACCG AGATTGAG 540
50 ACCCTGCTCT AGGGACCACC GACCCCCCG CCGGGAGGTA AGCTGGCCAG CGGTCTGTTT 600
CTGTCTGTCT CTGTCTTTGT GCGTGTGTTGT GCCGGCATCT AATGTTGCG CCTGCGTCTG 660
55 TACTAGTTAG CTAAGTAGCT CTGTATCTGG CGGACCCGTG GTGGAAGTGA CGAGTTCTGA 720
ACACCCGGCC GCAACCCTGG GAGACGTCCC AGGGACTTTG GGGGCCGTTT TTGTGGCCCC 780

	ACCTGAGGAA GGGAGTCGAT GTGGAATCCG ACCCCGTCAG GATATGTGGT TCTGGTAGGA	840
	GACGAGAACC TAAACAGTT CCCGCCTCCG TCTGAATTTT TGCTTTCGGT TTGGAACCGA	900
5	AGCCGCGCGT CTTGTCTGCT GCAGCGCTGC AGCATCGTTC TGTGTTCTCT CTGTCTGACT	960
	GTGTTTCTGT ATTGTCTGA AAATTAGGGC CAGACTGTTA CCACTCCCTT AAGTTTGACC	1020
10	TTAGGTCACT GGAAAGATGT CGAGCGGATC GCTCACAACC AGTCGGTAGA TGTCAAGAAG	1080
	AGACGTTGGG TTACCTTCTG CTCTGCAGAA TGGCCAACCT TTAACGTCGG ATGGCCGCGA	1140
	GACGGCACCT TTAACCGAGA CCTCATCACC CAGGTTAAGA TCAAGGTCTT TTCACCTGGC	1200
15	CCGCATGGAC ACCCAGACCA GGTCCCCTAC ATCGTGACCT GGGAAAGCCTT GGCTTTTGAC	1260
	CCCCCTCCCT GGGTCAAGCC CTTTGTAAC CTAAGCCTC CGCCTCCTCT TCCTCCATCC	1320
20	GCCCCGTCTC TCCCCCTTGA ACCTCCTCGT TCGACCCCGC CTCGATCCTC CCTTTATCCA	1380
	GCCCTCACTC CTTCTCTAGG CGCCGGAATT CCAGGACCAT GGGCGGGCCC CCTTAAACCA	1440
	TTAAATTGGT AAAATAAAGG ATCCGTCGAC CTGCAGCCAA GCTTATCGAT AAAATAAAAG	1500
25	ATTTTATTTA GTCTCCAGAA AAAGGGGGGA ATGAAAGACC CCACCTGTAG GTTTGGCAAG	1560
	CTAGCTTAAG TAACGCCATT TTGCAAGGCA TGGAAAATAC ATAACTGAGA ATAGAGAAGT	1620
30	TCAGATCAAG GTTAGGAACA GAGAGACAGC AGAATATGGG CCAAACAGGA TATCTGTGGT	1680
	AAGCAGTTCC TGCCCCGGCT CAGGGCCAAG AACAGATGGT CCCAGATGC GGTCCCGCCC	1740
	TCAGCAGTTT CTAGAGAACC ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAAATGAC	1800
35	CCTGTGCCTT ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCG CGCGCTTCTG	1860
	CTCCCCGAGC TCAATAAAAG AGCCCACAAC CCCTCACTCG GCGCGCCAGT CCTCCGATAG	1920
40	ACTGCGTCGC CCGGGTACCC GTGTATCCAA TAAACCCTCT TGCAGTTGCA TCCGACTTGT	1980
	GGTCTCGCTG TTCCTTGGGA GGGTCTCCTC TGAGTGATTG ACTACCCGTC AGCGGGGGTC	2040
	TTTCATTCTG AATCATGGTC ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GCTCACAATT	2100
45	CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCTT GGGGTGCCTA ATGAGTGAGC	2160
	TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTC AGTCGGGAAA CCTGTCTGTC	2220
50	CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT	2280
	TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGTTCGTTT GGCTGCGGCG AGCGGTATCA	2340
	GCTCACTCAA AGGCGGTAAAT ACGGTTATCC ACAGAAATCAG GGGATAACGC AGGAAAGAAC	2400
55	ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT	2460
	TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG	2520

	CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC	2580
	TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTTCTCCC TTCGGGAAGC	2640
5	GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT CCGTGTAGGT CGTTCGCTCC	2700
	AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC	2760
10	TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT	2820
	AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT	2880
	AACTACGGCT AACTAGAAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC	2940
15	TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAACAAA CCACCGCTGG TAGCGGTGGT	3000
	TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG GATCTCAAGA AGATCCTTTG	3060
20	ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAACT CACGTTAAGG GATTTTGGTC	3120
	ATGAGATTAT CAAAAGGAT CTTACCTAG ATCCTTTTAA ATTAAAAATG AAGTTTAA	3180
	TCAATCTAAA GTATATATGA GTAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG	3240
25	GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG TTGCCTGACT CCCCGTCGTG	3300
	TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA	3360
30	GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG	3420
	CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA	3480
	GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTACAGGC	3540
35	ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA	3600
	AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CCGTCCTCCG	3660
40	ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT	3720
	AATTCCTCTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGA CTGGTGA GTACTCAACC	3780
	AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCCGC GTCAATACGG	3840
45	GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCCTTCG	3900
	GGGCGAAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT	3960
50	GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA	4020
	GGAAGSCAAA ATGCCGCAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA	4080
	CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCAT GAGCGGATAC	4140
55	ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA	4200
	GTGCCACCTG ACGTCTAAGA AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT	4260

ATCACGAGGC CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG 4320
 CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG CCGGGAGCAG ACAAGCCCGT 4380
 5 CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCTGGC TTAACATATG GGCATCAGAG 4440
 CAGATTGTAC TGAGAGTGCA CCATATGCGG TGTGAAATAC CGCACAGATG CGTAAGGAGA 4500
 AAATACCGCA TCAGGCGCCA TTCGCCATTC AGGCTGCGCA ACTGTTGGGA AGGGCGATCG 4560
 10 GTGCGGGCCT CTTGCTATT ACGCCAGCTG GCGAAAGGGG GATGTGCTGC AAGGCGATTA 4620
 AGTTGGGTAA CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGCCACG 4680
 15 CTCTCCCTTA TCGACTCCT GCATTAGGAA GCAGCCCAGT AGTAGGTTGA GGCCGTTGAG 4740
 CACCGCCGCC GCAAGGAATG GTGCATGCAA GGAGATGGCG CCCAACAGTC CCCCGGCCAC 4800
 GGGGCTGCC ACCATACCCA CGCCGAAACA AGCGCTCATG AGCCCGAAGT GGCGAGCCCG 4860
 20 ATCTTCCCA TCGGTGATGT CGGCGATATA GGCGCCAGCA ACCGCACCTG TGGCGCCGGT 4920
 GATGCCGGCC ACGATGCGTC CGGCGTAGAG 4950

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 30 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Lys Lys Lys Arg Lys Val
 1 5

40 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 45 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
 1 5 10 15

55 Lys Lys Leu Asp
 20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Pro Pro
1

15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGGAAAGA AGAAGAAGAA GAAGAAGAAG AAGAAGGGGG GGCCCCCC

48

30 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTCCTCCTC CTCCTCCTCC TCCTCCTCT

30

(2) INFORMATION FOR SEQ ID NO:13:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
50 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 3..4

5 (D) OTHER INFORMATION: /note= "The 'N' appearing at position 3, as well as at positions 6, 9, 12, 15, 18, 21, 24, 27 and 30, can be either A,C,T or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 GGNGGGGGNG GNGGGGGNGG NGGNGGGNGN

30

(2) INFORMATION FOR SEQ ID NO:14:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 3..4

25 (D) OTHER INFORMATION: /note= "The 'N' appearing at position 3, as well as at positions 6, 9, 12, 15, 18, 21, 24, 27 and 30, can be either A, C, T or G."

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTTTTNT TTTTNTTNTT NTTNTTNTTN

30